WHAT IS CLAIMED IS:

1. A method for increasing net growth in a plant or seed, the method comprising applying an agent comprising lumichrome to the plant or seed in an amount effective for increasing net growth in the plant.

2. The method of claim 1, comprising applying the agent to a root, a shoot, a leaf, or a seed of the plant.

3. The method of claim 1, wherein the agent thus applied comprises a microorganism.

4. The method of claim 3, wherein the microorganism comprises a bacterium.

5. The method of claim 4, wherein the bacterium is an endophytic bacterium.

6. The method of claim 4, wherein the bacterium is a root-colonizing or shoot-colonizing bacterium.

7. The method of claim 3, wherein the microorganism is a soil-dwelling bacterium, a soil-dwelling yeast, or a soil-dwelling fungus.

8. The method of claim 4, wherein the bacterium is from the family *Rhizobiaceae,* a *Rhizobium spp.*, a *Bradyrhizobium spp*, a *Sinorhizobium spp.* or a *Pseudomonas spp.*

9. The method of claim 8, wherein the bacterium is a *Sinorhizobium fredii,* a *Sinorhizobium meliloti*, a *Bradyrhizobium japonicum,* or a *Pseudomonas fluorescens.*

10. The method of claim 4, wherein the bacterium is applied in an aqueous solution in a concentration of about 10^5 to about 10^{10} bacteria per mL.

11. The method of claim 10, wherein the bacterium is applied in an aqueous solution in a concentration of about 10^7 to about 10^8 bacteria per mL.

12. The method of claim 4, wherein the bacterium releases lumichrome at a rate of about 0.5 ng lumichrome/day/10^7 cells to about 10 ng lumichrome/day/10^7 cells.

13. The method of claim 1, wherein said agent thus applied comprises a bacteria culture media.

14. The method of claim 1, wherein said agent has a lumichrome concentration of about 3 nM to about 50 nM.

15. The method of claim 1, comprising applying said agent to said plant in multiple applications.

16. The method of claim 15, comprising applying to said agent to said plant about every 24 to 48 hours.

17. The method of claim 1, wherein said plant is an angiosperm.

18. The method of claim 17, wherein said angiosperm selected from the group consisting of monocotyledonous plants and dicotyledonous plants.

19. The method of claim 18, wherein said dicotyledonous plant is a legume.

20. The method of claim 19, wherein said legume is alfalfa.

21. A method for increasing net growth in a plant or seed, the method comprising growing the plant or seed in a hydroponic culture system comprising an aqueous medium comprising lumichrome or riboflavin in an amount effective for increasing net growth in the plant.

22. The method of claim 21, wherein the aqueous medium has a lumichrome concentration of about 3 nM to about 50 nM or riboflavin concentration of about 20 nM to about 500 nM.

23. A method for increasing net growth in a plant or seed, the method comprising growing the plant or seed in a controlled solid growth medium comprising a lumichrome-releasing or a riboflavin-releasing microorganism in an amount effective for increasing net growth in the plant.

24. The method of claim 23, wherein the medium has about 1 to about 20 micrograms of lumichrome per gram of medium, or about 10 to about 100 micrograms of riboflavin per gram of medium, or a concentration of lumichrome- or riboflavin-releasing microorganisms of about 10^5 to about 10^{10} bacteria per gram of medium.

25. The method of claim 23, wherein the medium is vermiculite, sterile vermiculite, peat, sterile peat, soil, or a sterile soil.

26. The method of claim 23, wherein the plant is a legume.

27. The method of claim 23, where a plant is growing in a medium under field conditions and the microorganism is inoculated onto the plant or seed or in the medium.

28. The method of claim 23, wherein the microorganism is a *Sinorhizobium meliloti* bacterium and the host plant is an alfalfa (*Medicago sativa*).

29. The method of claim 23, wherein the microorganism is a *Bradyrhizobium japonicum* bacterium and the host plant is a soybean (*Glycine max*).

30. The method of claim 23, wherein the microorganism is a *Sinorhizobium fredii* bacterium and the host plant is a soybean (*Glycine max*).

31. A method for increasing net growth in a plant, the method comprising applying to said plant an agent comprising a riboflavin-releasing or a lumichrome-releasing microorganism, wherein the microorganism is applied in an amount effective to increase net growth in the plant.

32. The method of claim 31, wherein the microorganism releases lumichrome or riboflavin at a rate of about 0.5 ng lumichrome or riboflavin/day/10^7 cells to about 2 ng lumichrome or riboflavin/day/10^7 cells.

33. The method of claim 31, wherein the microorganism thus applied has been selected or genetically engineered to release greater than wild type levels of lumichrome or riboflavin.

34. The method of claim 33, wherein the selected or genetically engineered microorganism releases riboflavin or lumichrome at a rate of about 2 ng lumichrome or riboflavin/day/10^7 cells to about 30 ng lumichrome or riboflavin/day/10^7 cells.

35. The method of claim 31, wherein the microorganism thus applied is an endophyte or a soil-dwelling microorganism.

36. The method of claim 31, wherein the microorganism thus applied is a bacterium.

37. The method of claim 36, wherein the bacterium is a *Sinorhizobium meliloti* bacterium and the host plant is a *Medicago spp.*

38. The method of claim 36, wherein the bacterium is a *Bradyrhizobium japonicum* bacterium and the host plant is a *Glycine max.*

39. The method of claim 36, wherein the bacterium is a *Sinorhizobium fredii* bacterium and the host plant is a *Glycine max.*

40. The method of claim 36, wherein the bacterium is from the family *Rhizobiaceae,* a *Rhizobium spp.*, a *Bradyrhizobium spp*, a *Sinorhizobium spp.* or a *Pseudomonas spp.*

41. The method of claim 40, wherein the bacterium is a *Sinorhizobium fredii,* a *Sinorhizobium meliloti*, a *Bradyrhizobium japonicum,* or a *Pseudomonas fluorescens.*

42. The method of claim 31, wherein the microorganism thus applied is a fungus.

43. The method of claim 42, wherein the fungus is an *Aspergillus*, a *Glomus*, a *Gigaspora*, or a *Scutellospora*.

44. The method of claim 31, wherein the microorganism thus applied is a yeast.

45. The method of claim 44, wherein the yeast is a *Candida*.

46. The method of claim 31, wherein the bacterium thus applied is in an aqueous solution in a concentration of about 10^5 to about 10^{10} bacteria per mL.

47. The method of claim 46, wherein the bacterium thus applied is in an aqueous solution in a concentration of about 10^7 to about 10^8 per mL.

48. The method of claim 33, wherein the microorganism thus selected or genetically engineered produces greater than wild-type levels of a riboflavin synthase or a protein effecting synthesis of riboflavin.

49. The method of claim 48, wherein the genetically engineered microorganism has been transduced with an expression cassette comprising a nucleic acid comprising a sequence substantially identical to SEQ ID NO:1.

50. The method of claim 48, wherein the genetically engineered microorganism has been transduced with an expression cassette comprising a nucleic acid encoding and expressing a riboflavin synthase or a protein effecting synthesis of riboflavin.

51. The method of claim 50, wherein the nucleic acid encoding a protein effecting synthesis of riboflavin is a coding sequence from a *ribC*, *ribD*, *ribBA*, *ribH* or *glyA* open reading frame.

52. The method of claim 51, wherein the *ribC* open reading frame is from *Escherichia coli* or *Sinorhizobium melioti*.

53. The method of claim 52, wherein the *ribC Sinorhizobium meliloti* open reading frame comprises a sequence substantially identical to SEQ ID NO:2.

54. The method of claim 53, wherein the *ribD Sinorhizobium meliloti* open reading frame comprises a sequence substantially identical to SEQ ID NO:4.

55. The method of claim 51, wherein the *glyA Sinorhizobium meliloti* open reading frame comprises a sequence substantially identical to SEQ ID NO:8.

56. The method of claim 51, wherein the *ribBA Sinorhizobium meliloti* open reading frame comprises a sequence substantially identical to SEQ ID NO:10.

57. The method of claim 51, wherein the *ribH Sinorhizobium meliloti* open reading frame comprises a sequence substantially identical to SEQ ID NO:12.

58. An isolated nucleic acid comprising a sequence substantially identical to or substantially complementary to a genomic sequence located in SEQ ID NO:1.

59. An expression cassette comprising the isolated nucleic acid of claim 58.

60. An transformed cell comprising the isolated nucleic acid of claim 58 or the expression cassette of claim 59.

61. An isolated nucleic acid comprising a nucleic acid sequence

having at least 65% sequence identity to SEQ ID NO:2 or a nucleic acid encoding a polypeptide, wherein the polypeptide has a sequence as set forth in SEQ ID NO:3; or

having at least 65% sequence identity to SEQ ID NO:4 or a nucleic acid encoding a polypeptide, wherein the polypeptide has a sequence as set forth in SEQ ID NO:5; or

having at least 65% sequence identity to SEQ ID NO:8 or a nucleic acid encoding a polypeptide, wherein the polypeptide has a sequence as set forth in SEQ ID NO:9; or

having at least 65% sequence identity to SEQ ID NO:10 or a nucleic acid encoding a polypeptide, wherein the polypeptide has a sequence as set forth in SEQ ID NO:11; or

which specifically hybridizes to SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:8 or SEQ ID NO:10 under stringent conditions, wherein the stringent conditions comprise at least one wash step using a solution comprising: a salt concentration of about 0.02 molar at pH 7 and a temperature of at least about 60°C, or a salt concentration of about 0.15 M NaCl at a temperature of about 72°C for about 15 minutes; or, a salt concentration of about 0.2X SSC at a temperature of at least about 50°C for about 15 minutes; or a salt concentration of about 2X SSC containing 0.1% SDS at room temperature for 15 minutes followed by a salt concentration of about by 0.1X SSC containing 0.1% SDS at 68°C for 15 minutes; or, equivalent conditions.

62. The nucleic acid of claim 61,

wherein the sequence identity to SEQ ID NO:2 is at least 75%; or
wherein the sequence identity to SEQ ID NO:4 is at least 75%; or
wherein the sequence identity to SEQ ID NO:8 is at least 75%; or
wherein the sequence identity to SEQ ID NO:10 is at least 75%.

63. The nucleic acid of claim 62,

wherein the sequence identity to SEQ ID NO:2 is at least 85%; or
wherein the sequence identity to SEQ ID NO:4 is at least 85%; or
wherein the sequence identity to SEQ ID NO:8 is at least 85%; or
wherein the sequence identity to SEQ ID NO:10 is at least 85%.

64. The nucleic acid of claim 63,

wherein the sequence identity to SEQ ID NO:2 is 95%; or
wherein the sequence identity to SEQ ID NO:4 is 95%; or
wherein the sequence identity to SEQ ID NO:8 is 95%; or
wherein the sequence identity to SEQ ID NO:10 is 95%.

65. The nucleic acid of claim 64,

wherein the nucleic acid comprises a sequence as set forth in SEQ ID NO:2; or
wherein the nucleic acid comprises a sequence as set forth in SEQ ID NO:4; or
wherein the nucleic acid comprises a sequence as set forth in SEQ ID NO:8; or
wherein the nucleic acid comprises a sequence as set forth in SEQ ID NO:10.

66. An expression cassette comprising at least one nucleic acid of claim 61 operably linked to a transcriptional regulatory sequence.

67. A transformed cell comprising at least one nucleic acid of claim 61 or the expression cassette of claim 66.

68. The transformed cell of claim 67, wherein the cell is a microorganism.

69. The transformed cell of claim 68, wherein the microorganism is a soil-dwelling or a plant endophytic microorganism.

70. The transformed cell of claim 69, wherein the microorganism is a bacterium.

71. The transformed cell of claim 70, wherein the bacterium from the family *Rhizobiaceae*, a *Rhizobium spp.*, a *Bradyrhizobium spp*, a *Sinorhizobium spp.* or a *Pseudomonas spp.*

72. The transformed cell of claim of claim 71, wherein the bacterium is a *Sinorhizobium fredii*, a *Sinorhizobium meliloti*, a *Bradyrhizobium japonicum*, or a *Pseudomonas fluorescens*.

73. The transformed cell of claim 68, wherein the microorganism is a fungus.

74. The transformed cell of claim 73, wherein the fungus is an *Aspergillus*, a *Glomus*, a *Gigaspora*, or a *Scutellospora*.

75. The transformed cell of claim 68, wherein the microorganism is a yeast.